

What is claimed is:

1. A three-dimensional model selected from the group consisting of: (a) a three-dimensional model of a complex between (i) an extracellular domain of a human high affinity Fc epsilon receptor alpha chain (Fc $\epsilon$ RI $\alpha$ ) protein and (ii) a human IgE Fc 5 region comprising C $\epsilon$ 3 and C $\epsilon$ 4 domains (Fc-C $\epsilon$ 3/C $\epsilon$ 4), wherein said model substantially represents the atomic coordinates specified in Table 1; and (b) a three-dimensional model comprising a modification of said model of (a), wherein said modification represents a complex between a Fc receptor protein that binds to a Fc domain of an antibody and an antibody Fc region that binds to a Fc receptor protein. the hinge between domain C $\epsilon$ 3 and 10 domain C $\epsilon$ 4 of the Fc-C $\epsilon$ 3/C $\epsilon$ 4 region, and a Fc $\epsilon$ RI $\alpha$ :Fc-C $\epsilon$ 3/C $\epsilon$ 4 region that interacts with 3-[3-(cholamidopropyl) dimethylammonio]-1-propane-sulfonate (CHAPS).

2. A method to produce the three-dimensional model of claim 1, wherein the three-dimensional model is the complex between the extracellular domain of a human Fc $\epsilon$ RI $\alpha$  protein and a human Fc-C $\epsilon$ 3/C $\epsilon$ 4 region, said method comprising representing 15 amino acids of said protein and said region in said complex at substantially the atomic coordinates specified in Table 1.

3. A method to produce the three-dimensional model of a complex between  
(i) an extracellular antibody binding domain of an antibody receptor protein other than  
human Fc $\epsilon$ RI $\alpha$  as represented by coordinates in Table 1 and (ii) an antibody receptor  
binding domain of an antibody other than human IgE as represented by coordinates in  
5 Table 1, said method comprising homology modeling.

4. An isolated crystal of a complex between an extracellular domain of a Fc $\epsilon$ RI $\alpha$  protein and an IgE Fc-C $\epsilon$ 3/C $\epsilon$ 4 region.
5. A method to produce the isolated crystal of claim 4, wherein the complex is between an extracellular domain of a Fc $\epsilon$ RI $\alpha$  protein and an IgE Fc-C $\epsilon$ 3/C $\epsilon$ 4 region,  
5 said method comprising vapor diffusion.

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6. A method to identify a compound that inhibits the binding between an IgE antibody and a Fc $\epsilon$ RI $\alpha$  protein, said method comprising using a three-dimensional model of a complex between an extracellular domain of a human high affinity Fc $\epsilon$ RI $\alpha$  protein and a human Fc-C $\epsilon$ 3/C $\epsilon$ 4 region to identify said compound, wherein said model  
5 substantially represents the atomic coordinates specified in Table 1.

7. An inhibitory compound identified in accordance with the method of  
Claim 6.

8. A therapeutic composition comprising an inhibitory compound of Claim 7.

9. A method to protect an animal from allergy, said method comprising  
10 administering to said animal an inhibitory compound of Claim 7.

10. A compound that inhibits the binding between an IgE antibody and a Fc $\epsilon$ RI $\alpha$  protein, said compound identified by analysis of a three-dimensional model of a complex between an extracellular domain of a human high affinity Fc $\epsilon$ RI $\alpha$  protein and a human Fc-C $\epsilon$ 3/C $\epsilon$ 4 region to identify said compound, wherein said model substantially  
5 represents the atomic coordinates specified in Table 1.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

11. A polypeptide selected from the group consisting of a Fc $\epsilon$ RI $\alpha$ :Fc-C $\epsilon$ 3/C $\epsilon$ 4 interaction site 1, a Fc $\epsilon$ RI $\alpha$ :Fc-C $\epsilon$ 3/C $\epsilon$ 4 interaction site 2, a C strand of domain 2 of Fc $\epsilon$ RI $\alpha$ , a C'E loop of domain 2 of Fc $\epsilon$ RI $\alpha$ , a tryptophan-containing hydrophobic ridge of Fc $\epsilon$ RI $\alpha$ , a crystal contact cluster involved in IgE binding; a FG loop in D2; a D1D2 interface; a cleft between D1 and D2; a domain 1; a domain 2; a hydrophobic core; a A'B loop of D1; a EF loop of D1; a BC loop of D2; a CC' loop of D2; and a strand of D2.

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12. An isolated nucleic acid molecule encoding the polypeptide of Claim 11.

13. A method of using the three-dimensional model of claim 1, comprising:

10 (a) analyzing the three-dimensional model substantially representing the atomic coordinates specified in Table 1 to identify at least one amino acid of a target protein represented by said three-dimensional model which if replaced by said identified amino acid(s) to improve a function of said target protein; and

15 (b) replacing said identified amino acid(s) to produce a mutein having at least one of said improved function.

14. The method of claim 13, wherein said target protein is a Fc-C $\epsilon$ 3/C $\epsilon$ 4 protein, a Fc $\epsilon$ RI $\alpha$  protein or a protein comprising SEQ.ID NO.2, and wherein said improved function is selected from the group comprising: (a) increased stability, increased affinity for an IgE binding domain of a Fc $\epsilon$ RI $\alpha$  protein, altered substrate specificity or increased solubility when said target protein is the Fc-C $\epsilon$ 3/C $\epsilon$ 4 protein; and

20 (b) increased stability, increased affinity for an Fc-domain of an antibody, altered substrate specificity or increased stability when said target protein is the Fc $\epsilon$ RI $\alpha$  protein or the protein comprising SEQ.ID NO.2.

15. A mutein produced by the method of claim 14, wherein said mutein has at least one improved function compared to the target protein, wherein said target protein is the Fc $\epsilon$ RI $\alpha$  protein, the Fc-C $\epsilon$ 3/C $\epsilon$ 4 protein or the protein comprising SEQ.ID NO.2.

16. The mutein of claim 15 having an improved function compared to an unmodified Fc $\epsilon$ RI $\alpha$  protein, wherein the amino acid sequence of said mutein differs in at least one position from the amino acid sequence of said unmodified protein, said position being in a region selected from the group consisting of a crystal contact cluster, a tryptophan-containing hydrophobic ridge, a FG loop in D2, a D1D2 interface, a cleft between D1 and D2, a domain 1, a domain 2, a hydrophobic core, a A'B loop of D1, a EF loop of D1, a BC loop of D2, a C strand of D2, a CC' loop of D2, a C'E loop of D2, a strand of D2, the amino terminal five residues of said protein, and the carboxyl terminal five residues of said protein.

17. An isolated nucleic acid sequence encoding a mutein of Claim 15.

18. A recombinant virus comprising said nucleic acid sequence of Claim 17.

15 19. A recombinant cell comprising said nucleic acid sequence of Claim 17, wherein said cell is capable of expressing said nucleic acid sequence.

20. A diagnostic reagent comprising a mutein of Claim 15.

21. A therapeutic composition comprising a mutein of Claim 15.

22. A method to use a mutein of Claim 15, wherein said method is selected from the group consisting of: (a) a method to protect an animal from allergy, said method comprising administering a therapeutic composition comprising said mutein to said animal; (b) a method to detect allergy, or susceptibility thereto, in an animal, said method

comprising using said mutein to detect said allergy; and (c) a method to enhance the performance of an IgE binding assay, said method comprising incorporating into said assay said mutein.